

SEQUENCE LISTING

&lt;110&gt; PHARMA PACIFIC PTY LTD

&lt;120&gt; INTERFERON-ALPHA INDUCED GENE

&lt;130&gt; N.86243A JCI

&lt;160&gt; 4

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 8157

&lt;212&gt; DNA

&lt;213&gt; HOMO SAPIENS

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(5902)

&lt;223&gt;

&lt;400&gt; 1

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				1 5	

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Ser Phe Pro Leu Leu Val Glu Gly Ser Trp Gly Pro Asp Pro Pro Lys	
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Asn Leu Asn Thr Lys Leu Gln Met Tyr Phe Gln Ser Pro Lys Arg Ser	
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Gly Gly Gly Glu Cys Glu Val Arg Gln Asp Pro Arg Ser Pro Ser Arg	
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His Gly Arg Val Thr Arg Pro Thr Ser Ala Ala Ala Val Ala Glu Ala	
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Leu Ser Leu Asp Arg Phe Leu Ser Phe Pro Val Val Val Val Leu Leu	
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gat act tcc aca aca ctc tct agc atc agg tct aaa tat aaa gtc aac Asp Thr Ser Thr Thr Leu Ser Ser Ile Arg Ser Lys Tyr Lys Val Asn 520 525 530	1699
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acc agc tgt tct tct gaa gcc ctg tta gaa gca gaa aag caa atg ctc Thr Ser Cys Ser Ser Glu Ala Leu Leu Glu Ala Glu Lys Gln Met Leu 710 715 720 725	2275
agt gcc tta aat tat aag cgc att gaa gtt gag aac aaa gaa gtt ctt Ser Ala Leu Asn Tyr Lys Arg Ile Glu Val Glu Asn Lys Glu Val Leu 730 735 740	2323
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gtg ctc aaa Val Leu Lys 1210	acc agc agc tgg aat Thr Ser Ser Trp Asn 1215	ctg gac tgt cgc tat Leu Asp Cys Arg Tyr 1220	gtg ctt Val Leu	3766

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aag ata atg Lys Ile Met 1240	gaa gac ata atc aga Glu Asp Ile Ile Arg 1245	gaa tgt atg gag atc act gag Glu Cys Met Glu Ile Thr Glu 1250	3856
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aac ttg gga Asn Leu Gly 1270	ttt cct aaa aac ata Phe Pro Lys Asn Ile 1275	ttc gct gaa tta atc att tca Phe Ala Glu Leu Ile Ile Ser 1280	3946
gag gtg ttc Glu Val Phe 1285	aaa ttt agt agc aag Lys Phe Ser Ser Lys 1290	aat cag ctg aaa act tta caa Asn Gln Leu Lys Thr Leu Gln 1295	3991
gag gtt cac Glu Val His 1300	ttt ctg ctg cac ccg Phe Leu Leu His Pro 1305	agt gat cat gaa aat att cag Ser Asp His Glu Asn Ile Gln 1310	4036
gca ttt tca Ala Phe Ser 1315	gat gaa ttt gcc aga Asp Glu Phe Ala Arg 1320	agg gct aat gga aat ctc gtc Arg Ala Asn Gly Asn Leu Val 1325	4081
agt gac aaa Ser Asp Lys 1330	att ccg aag gct aaa Ile Pro Lys Ala Lys 1335	gat aca caa ggt ttt tat ggg Asp Thr Gln Gly Phe Tyr Gly 1340	4126
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gac aat aac Asp Asn Asn 1675	act tct cat tgt ttt Thr Ser His Cys Phe 1680	aac aaa atg acc aat Asn Lys Met Thr Asn 1685	ctg aaa Leu Lys	5161
tta gag gat Leu Glu Asp 1690	gca agg aga gaa aag Ala Arg Arg Glu Lys 1695	aaa aaa aca gtt gat Lys Lys Thr Val Asp 1700	gtc aaa Val Lys	5206
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tcc aaa gtt Ser Lys Val 1735	gac atc cct gca cac Asp Ile Pro Ala His 1740	tgg agt gat atg aag Trp Ser Asp Met Lys 1745	cag cag Gln Gln	5341
aat ttc tgt Asn Phe Cys 1750	gtg gtg gag ctg ctg Val Val Glu Leu Leu 1755	cct agt gat cct gag Pro Ser Asp Pro Glu 1760	tac aac Tyr Asn	5386
acg gtg gca Thr Val Ala 1765	agc aag ttt aat cag Ser Lys Phe Asn Gln 1770	acc tgc tca cac ttc Thr Cys Ser His Phe 1775	aga ata Arg Ile	5431
gag aag att Glu Lys Ile 1780	gag agg atc cag aat Glu Arg Ile Gln Asn 1785	cca gat ctc tgg aat Pro Asp Leu Trp Asn 1790	agc tac Ser Tyr	5476
cag gca aag Gln Ala Lys 1795	aaa aaa act atg gat Lys Lys Thr Met Asp 1800	gcc aag aat ggc cag Ala Lys Asn Gly Gln 1805	aca atg Thr Met	5521
aat gag aag Asn Glu Lys 1810	caa ctc ttc cat ggg Gln Leu Phe His Gly 1815	aca gat gcc ggc tcc Thr Asp Ala Gly Ser 1820	gtg cca Val Pro	5566
cac gtc aat His Val Asn 1825	cga aat ggc ttt aac Arg Asn Gly Phe Asn 1830	cgc agc tat gcc gga Arg Ser Tyr Ala Gly 1835	aag aat Lys Asn	5611
gct gtg gca Ala Val Ala 1840	tat gga aag gga acc Tyr Gly Lys Gly Thr 1845	tat ttt gct gtc aat Tyr Phe Ala Val Asn 1850	gcc aat Ala Asn	5656

tat tct gcc	aat gat acg tac tcc	aga cca gat gca aat	ggg aga	5701		
Tyr Ser Ala	Asn Asp Thr Tyr Ser	Arg Pro Asp Ala Asn	Gly Arg			
1855	1860	1865				
aag cat gtg	tat tat gtg cga gta	ctt act gga atc tat	aca cat	5746		
Lys His Val	Tyr Tyr Val Arg Val	Leu Thr Gly Ile Tyr	Thr His			
1870	1875	1880				
gga aat cat	tca tta att gtg cct	cct tca aag aac cct	caa aat	5791		
Gly Asn His	Ser Leu Ile Val Pro	Pro Ser Lys Asn Pro	Gln Asn			
1885	1890	1895				
cct act gac	ctg tat gac act gtc	aca gat aat gtg cac	cat cca	5836		
Pro Thr Asp	Leu Tyr Asp Thr Val	Thr Asp Asn Val His	His Pro			
1900	1905	1910				
agt tta ttt	gtg gca ttt tat gac	tac caa gca tac cca	gag tac	5881		
Ser Leu Phe	Val Ala Phe Tyr Asp	Tyr Gln Ala Tyr Pro	Glu Tyr			
1915	1920	1925				
ctt att acg	ttt aga aaa taa cactttgga	tccttccac	aaaattattc	5932		
Leu Ile Thr	Phe Arg Lys					
1930						
tccatttgta	catatctagt	tgtaaaacaa	gttttagctt	ttttttttaa	ttcctcttaa	5992
cagatttttc	taatatccaa	ggatcattct	ttgtcgctgc	agtcagctct	tcttcagctt	6052
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Glu Gly 1520	Thr Gln Leu Ser Ser 1525	Gln Gln Ser Val Met 1530	Ser Lys Leu
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His Leu 1550	Val Leu Glu Lys Lys 1555	Thr Glu Ser Ala Thr 1560	Phe Arg Val
Cys Gly 1565	Glu Asn Val Thr Cys 1570	Val Glu Tyr Ala Ile 1575	Ser Trp Leu
Gln Asp 1580	Leu Ile Glu Lys Glu 1585	Gln Cys Pro Tyr Thr 1590	Ser Glu Asp
Glu Cys 1595	Ile Lys Asp Phe Asp 1600	Glu Lys Glu Tyr Gln 1605	Glu Leu Asn
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Thr Asn 1685	Leu Lys Leu Glu Asp 1690	Ala Arg Arg Glu Lys 1695	Lys Lys Thr
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18

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23

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Met Asn Leu Pro Arg Arg Val Lys Glu Asn Leu Val Ser Asp Lys Phe  
1 5 10 15

Pro Lys Ala Lys Asp Thr Gln Gly Phe Tyr Gly Thr Val Ser Ser Pro  
20 25 30

Asp Ser Gly Val Tyr Glu Met Lys Ile Gly Ser Ile Ile Phe Gln Val  
35 40 45

Ala Ser Gly Asp Ile Thr Lys Glu Glu Ala Asp Val Ile Val Asn Ser  
50 55 60

Thr Ser Asn Ser Phe Asn Leu Lys Ala Gly Val Ser Lys Ala Ile Leu  
65 70 75 80

Glu Cys Ala Gly Gln Asn Val Glu Arg Glu Cys Ser Gln Gln Ala Gln  
85 90 95

Gln Arg Lys Asn Asp Tyr Ile Ile Thr Gly Gly Gly Phe Leu Arg Cys  
100 105 110

Lys Asn Ile Ile His Val Ile Gly Gly Asn Asp Val Lys Ser Ser Val  
115 120 125

Ser Ser Val Leu Gln Glu Cys Glu Lys Lys Asn Tyr Ser Ser Ile Cys  
130 135 140

Leu Pro Ala Ile Gly Thr Gly Asn Ala Lys Gln His Pro Asp Lys Val  
145 150 155 160

Ala Glu Ala Ile Ile Asp Ala Ile Glu Asp Phe Val Gln Lys Gly Ser  
165 170 175

Ala Gln Ser Val Lys Lys Val Lys Val Val Ile Phe Leu Pro Gln Val  
180 185 190

Leu Asp Val Phe Tyr Ala Asn Met Lys Lys Arg Glu Gly Thr Gln Leu  
195 200 205

Ser Ser Gln Gln Ser Val Met Ser Lys Leu Ala Ser Phe Leu Gly Phe  
210 215 220

Ser Lys Gln Ser Pro Gln Lys Lys Asn His Leu Val Leu Glu Lys Lys  
 225 230 235 240  
 Thr Glu Ser Ala Thr Phe Arg Val Cys Gly Glu Asn Val Thr Cys Val  
 245 250 255  
 Glu Tyr Ala Ile Ser Trp Leu Gln Asp Leu Ile Glu Lys Glu Gln Cys  
 260 265 270  
 Pro Tyr Thr Ser Glu Asp Glu Cys Ile Lys Asp Phe Asp Glu Lys Glu  
 275 280 285  
 Tyr Gln Glu Leu Asn Glu Leu Gln Lys Lys Leu Asn Ile Asn Ile Ser  
 290 295 300  
 Leu Asp His Lys Arg Pro Leu Ile Lys Val Leu Gly Ile Ser Arg Asp  
 305 310 315 320  
 Val Met Gln Ala Arg Asp Glu Ile Glu Ala Met Ile Lys Arg Val Arg  
 325 330 335  
 Leu Ala Lys Glu Gln Glu Ser Arg Ala Asp Cys Ile Ser Glu Phe Ile  
 340 345 350  
 Glu Trp Gln Tyr Asn Asp Asn Asn Thr Ser His Cys Phe Asn Lys Met  
 355 360 365  
 Thr Asn Leu Lys Leu Glu Asp Ala Arg Arg Glu Lys Lys Lys Thr Val  
 370 375 380  
 Asp Val Lys Ile Asn His Arg His Tyr Thr Val Asn Leu Asn Thr Tyr  
 385 390 395 400  
 Thr Ala Thr Asp Thr Lys Gly His Ser Leu Ser Val Gln Arg Leu Thr  
 405 410 415  
 Lys Ser Lys Val Asp Ile Pro Ala His Trp Ser Asp Met Lys Gln Gln  
 420 425 430  
 Asn Phe Cys Val Val Glu Leu Leu Pro Ser Asp Pro Glu Tyr Asn Thr  
 435 440 445  
 Val Ala Ser Lys Phe Asn Gln Thr Cys Ser His Phe Arg Ile Glu Lys  
 450 455 460  
 Ile Glu Arg Ile Gln Asn Pro Asp Leu Trp Asn Ser Tyr Gln Ala Lys  
 465 470 475 480  
 Lys Lys Thr Met Asp Ala Lys Asn Gly Gln Thr Met Asn Glu Lys Gln  
 485 490 495  
 Leu Phe His Gly Thr Asp Ala Gly Ser Val Pro His Val Asn Arg Asn  
 500 505 510



Gly Phe Asn Arg Ser Tyr Ala Gly Lys Asn Ala Val Ala Tyr Gly Lys  
515 520 525

Gly Thr Tyr Phe Ala Val Asn Ala Asn Tyr Ser Ala Asn Asp Thr Tyr  
530 535 540

Ser Arg Pro Asp Ala Asn Gly Arg Lys His Val Tyr Tyr Val Arg Val  
545 550 555 560

Leu Thr Gly Ile Tyr Thr His Gly Asn His Ser Leu Ile Val Pro Pro  
565 570 575

Ser Lys Asn Pro Gln Asn Pro Thr Asp Leu Tyr Asp Thr Val Thr Asp  
580 585 590

Asn Val His His Pro Ser Leu Phe Val Ala Phe Tyr Asp Tyr Gln Ala  
595 600 605

Tyr Pro Glu Tyr Leu Ile Thr Phe Arg Lys  
610 615